BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

SEQ ID NO: 8

Results for: |lcl|55839 None(22bp) ▾|
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
lcl|55839
Description
None
Molecule type
nucleic acid
Query Length
22

Subject ID
gi|1914699|emb|X98077.1|
Description
Hepatitis B virus complete genome, wild type
Molecule type
nucleic acid
Subject Length
3215
Program
BLASTN 2.2.22+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

| Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Effective search space 48120

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Graphic Summary

Distribution of 8 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.
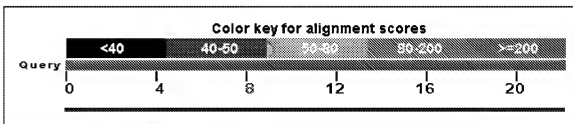
Dot Matrix View

Plot of lcl|55839 vs gi|1914699|emb|X98077.1| [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: 🅤 UniGene 🄴 GEO 🄶 Gene 🕸 Structure 🅜 Map Viewer

```
Sequences producing significant alignments:
(Click headers to sort columns)
X98077.1  Hepatitis B virus complete genome, wild type        44.1   148   100%   3e-09 100%
```

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Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>emb|X98077.1| Hepatitis B virus complete genome, wild type
Length=3215

Sort alignments for this subject seq
E value **Score** Percent identity
Query start position Subject star

```
 Score = 44.1 bits (22),  Expect = 3e-09
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Minus

Query  1     GGAGTCCGCGTAAAGAGAGGTG  22
             ||||||||||||||||||||||
Sbjct  1548  GGAGTCCGCGTAAAGAGAGGTG  1527


 Score = 16.4 bits (8),  Expect = 0.58
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Minus

Query  12    AAAGAGAG  19
             ||||||||
Sbjct  1953  AAAGAGAG  1946


 Score = 16.4 bits (8),  Expect = 0.58
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Plus

Query  12    AAAGAGAG  19
             ||||||||
Sbjct  2782  AAAGAGAG  2789


 Score = 14.4 bits (7),  Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  1     GGAGTCC  7
             |||||||
Sbjct  179   GGAGTCC  173


 Score = 14.4 bits (7),  Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  4     GTCCGCG  10
             |||||||
Sbjct  1455  GTCCGCG  1449


 Score = 14.4 bits (7),  Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  16    AGAGGTG  22
             |||||||
Sbjct  1598  AGAGGTG  1592


 Score = 14.4 bits (7),  Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
```

```
  Strand=Plus/Minus

Query  16      AGAGGTG  22
               |||||||
Sbjct  1832    AGAGGTG  1826


 Score = 14.4 bits (7),   Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
  Strand=Plus/Minus

Query  16      AGAGGTG  22
               |||||||
Sbjct  3182    AGAGGTG  3176
```

Select All Get selected sequences Distance tree of results Multiple alignment   NEW